Vivaldi Project

Data management plan

Crassostrea gigas response to OsHV-1 and vibrios (Harveyi clade)

Dual RNAseq
Oyster response to vibrios in the presence/absence of OsHV-1

04/02/2020

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	*CNRS*
Data category	*Transcriptome (host)*
Concerned WP	*WP2*
Name of the VIVALDI referent(s)	*Transcriptome: Beatriz Novoa & Paola Venier*
Reference of the dataset *Please refer to the DMP table to find the appropriate reference.* *Ex: Genome-Patho/SubTaskN°/Pathogen/PartnerN°*	*Transcriptome-host/2.1.1/oyster/CNRS_IHPE*
Description of the data	The response of oysters *C. gigas* to virulent/non-virulent vibrios was evaluated by RNAseq on oysters infected with a consortium of 18 strains of the Harveyi clade in the presence/absence of OsHV-1 virus. Material was one full-sib family of oysters susceptible to wild infections. The oyster and bacterial responses to infection were compared before mortalities occurrence and 4h, 24h and 48h after infection.
Type	*Sequences*
Period and frequency of data collection	Control and treated oysters sampled at 4, 24 and 48 h after infection
Geographical site of data collection (if applicable)	*France*
Description of the material from which the dataset is generated *Information will be obtained from individuals, which can come from natural/hatchery population and/or from family produced in hatchery. Animals can be infected (naturally or experimentally). DNA extraction can be done from the whole animal, tissue.*	*A biparental family of oysters (La Tremblade #H12). Whole tissues.*
Protocols *Example: 16S ribosomal RNA gene sequencing by NGS* ***Please refer to the DMP table* for more examples***	*NGS sequencing of ribo-depleted RNA (Nugen technology) extracted from infected and non-infected oysters. Sequencing Novaseq 2x50 bp. Fasteris.*
Nature of the collected/generated data	*fastq*

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Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed datas set will be .vcf/.bed formats. ***Please refer to the DMP table* for more examples***	
Coverage (if applicable) *Example: random genomic regions covered at 50 X* ***Please refer to the DMP table* for more examples***	*100 millions paired-end reads per sample*
What are the prerequisites allowing to use the data as such? *Example: Any person able to use .fastqc file and .fasta file* ***Please refer to the DMP table* for more examples***	*Any person able to use .fastqc file and .fasta file*
Sharing of main data	*Saved and shared after publication*
Archiving and preservation *Example: data will be stored on a hard drive + online back up and then will be released on public database (Sinoe, Dryad) after publication.* ***Please refer to the DMP table* for more examples***	*SRA database*
List, description and storage of associated data (metadata) *Examples: environmental data, mortality monitoring, genotyping…*	
Sharing of metadata (if relevant)	*No relevant*

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